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Om nucleic - nucleic search, using bw model.

Run on: January 24, 2006, 05:25:18 ; Search time 1497 Seconds
(without alignments)

9793.993 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1973

Sequencing table: IDENTITY NUC Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1773	100.0	1773	Sequence 2, Appli
c 3	1285.2	72.5	8	Sequence 2, Appli
c 4	1278.8	72.1	1768	Sequence 4, Appli
c 5	1277.2	72.0	1768	Sequence 2, Appli
c 6	1274.9	71.9	1768	Sequence 6, Appli
c 7	1274.71.9	71.9	1768	Sequence 3, Appli
c 8	1218.2	68.7	1762	Sequence 5, Appli
c 9	1198.8	67.5	1759	Sequence 1, Appli
c 10	1198.8	67.4	7460	Sequence 7, Appli
c 11	1195.8	67.4	5225	Sequence 16, Appli
c 12	1195.8	67.4	5285	Sequence 1, Appli
c 13	1195.8	67.4	5650	Sequence 2, Appli
c 14	1195.8	67.4	5650	Sequence 17, Appli
c 15	1059.8	59.8	1759	Sequence 5, Appli
c 16	1059.8	59.8	1759	Sequence 5, Appli
c 17	1059.8	59.8	1759	Sequence 5, Appli
c 18	1059.8	59.8	1759	Sequence 5, Appli
c 19	1059.4	59.7	1768	Sequence 1, Appli
c 20	1059.4	59.7	1768	Sequence 1, Appli
c 21	981.2	55.3	1768	Sequence 3, Appli
c 22	981.2	55.3	1768	Sequence 3, Appli
c 23	981.2	55.3	1768	Sequence 3, Appli

RESULT 1
US-10-314-512-2

; Sequence 2, Application US/10314512

; Publication No. US20030170270A1

; GENERAL INFORMATION:

; APPLICANT: Meng, Xiang-Jin

; APPLICANT: Fenaux, Martijn

; APPLICANT: Halbur, Patrick G.

; TITLE OF INVENTION: Chimeric Infectious DNA Clones, Chimeric Porcine Circoviruses and FILE REFERENCE: AM100878

; CURRENT APPLICATION NUMBER: US/10/314-512

; CURRENT FILING DATE: 2002-12-09

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1773

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-10-314-512-2

RESULT 1
US-10-314-512-2

; Sequence 2, Application US/10314512

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; LENGTH: 1773

; TYPE: DNA

; ORGANISM: Porcine circovirus

US-10-314-512-2

ALIGNMENTS

Query Match 100.0%; Score 1773; DB 6; Length 1773;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1773; Conservative 0;

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Db 1 GTGACTCGTGTGATGGTCTCAGCAGTCAGTAAATTGCAAGTAGTAATCCCTCCGA, 60

Qy 61 TAGAGAGCTTCACTACGTGGCACAGCAGTTGAGGATACCCCTTAATGTCCTACAGTC 120

Db 61 TAGAGAGCTTCACTACGTGGCACAGCAGTTGAGGATACCCCTTAATGTCCTACAGTC

Qy 121 CNGTAACTCAAATACTCNGGCCAAAAAAGAACGTAACGTTCTACAGTC 180

Db 121 CNGTAACTCAAATACTCNGGCCAAAAAAGAACGTAACGTTCTACAGTC

Qy 181 ATGGATACCGGTCAAGTCAGTAACTCCAGGTAACCGCATAAATCA 240

Db 181 ATGGATACCGGTCAAGTCAGTAACTCCAGGTAACCGCATAAATCA

Qy 241 TCCAAACAAACACTCTCTCCATGATATCCACCACTTACTGGCTTC 300

Db 241 TCCAAACAAACACTCTCTCCATGATATCCACCACTTACTGGCTTC

Qy 301 CAGTAGGTGTCCCTAGSCTCAGCAAATTACGGCCGACTGGCTCTCCACACCGGGC 360

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 05:06:16 ; Search time 333 Seconds

(without alignments)
 9464.315 Million cell updates/sec

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 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 9: /cn2_6/podata/1/ina/backfiles.seq/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 4	1059.8	59.8	1759	3	US-09-583-350-3
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C 6	1059.8	59.8	1759	3	US-09-884-514-3
C 7	1053.2	59.4	3609	3	US-09-784-962-5
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C 10	981.2	55.3	1768	3	US-09-082-558-3
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C 12	981.2	55.3	1768	3	US-09-884-514-4
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C 15	976.4	55.1	1768	3	US-09-082-558-4
C 16	976.4	55.1	1768	3	US-09-161-092-4
C 17	976.4	55.1	1768	3	US-09-583-350-4
C 18	976.4	55.1	1768	3	US-09-884-514-4
C 19	976.4	55.1	1768	3	US-09-784-962-4
C 20	967.2	54.6	1768	3	US-09-161-092-6
C 21	967.2	54.6	1768	3	US-09-161-092-6
C 22	967.2	54.6	1768	3	US-09-583-350-6
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Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
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c 20	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DR179060	RTWNT1_1	DR179060 RTWNT1_1
c 21	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DR012815	HRAT1_15	DR012815 HRAT1_15
c 22	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DN458173	EST933972	DN458173 EST933972

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OM nucleic - nucleic search, using bw model

Run on: January 24, 2006, 05:14:52 ; Search time 7316 Seconds
(without alignments)

11338.641 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggttaacctccgtggattgttc.....caaatcgcccttcgggtacc 1773 ,

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

RESULT 1

CNS00LT2/c
LOCUS CNS00LT2/c
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR8P19 of RP1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL078714
VERSION AL078714.1 GI:5102004
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydriidae; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Genoscope
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 FRAY cedex - FRANCE (E-mail : seeref@genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammober in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.him.

FEATURES Location/Qualifier
Source .1..1101
/organism="Drosophila melanogaster"
/mol_type="Genomic DNA"
/db_xref="taxon:727"
/clone_id="RPCI-98"
/clone_label="RPCI-98"
/note="end : TET3"

ALIGNMENTS

c 23	45.2	2.5	CV144191	BST855400
c 24	45.2	2.5	DR09500	RTALL_9_C
c 25	45.2	2.5	DN45245	DN45245
c 26	27	45.2	DN447345	DN447345
c 27	45.2	2.5	DN46355	DN46355
c 28	45.2	2.5	DN460355	DN460355
c 29	45.2	2.5	CV138441	CV138441
c 30	45.2	2.5	DN458986	DN458986
c 31	45.2	2.5	CN784300	BST72991
c 32	45.2	2.5	DN447213	DN447213
c 33	45.2	2.5	DN452364	DN452364
c 34	45.2	2.5	DN460425	DN460425
c 35	45.2	2.5	DN449051	DN449051
c 36	45.2	2.5	CV137577	CV137577
c 37	45.2	2.5	CV146884	CV146884
c 38	45.2	2.5	DN453011	DN453011
c 39	45.2	2.5	CO413802	CO413802
c 40	45.2	2.5	DN451000	DN451000
c 41	45.2	2.5	CO409276	CO409276
c 42	45.2	2.5	DN451374	DN451374
c 43	45.2	2.5	CO410601	CO410601
c 44	45.2	2.5	CV138839	CV138839
c 45	45.2	2.5	CO413933	CO413933

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
c 1	56.6	EST:*	1: gb_est1:*	3.2	CNS00LT2	AL078714	Drosophil	AL078714 Drosophil
c 2	50.9	EST:*	2: gb_est2:*	2.8	CNS00LT2	AL059400	Drosophil	AL059400 Drosophil
c 3	48.6	EST:*	3: gb_est3:*	2.7	CNS00LT2	BG445569	GA_Ba002	BG445569 GA_Ba002
c 4	48.2	EST:*	4: gb_htc:*	2.7	CNS00LT2	CD659610	StBSPref53	CD659610 StBSPref53
c 5	47.6	EST:*	5: gb_est4:*	2.7	CNS00LT2	AG665778	Mus_muscu	AG665778 Mus_muscu
c 6	47.4	EST:*	6: gb_est5:*	2.7	CNS00LT2	AL066784	Drosophil	AL066784 Drosophil
c 7	47.2	EST:*	7: gb_est6:*	2.7	CNS00LT2	AG886740	Oryza_sat	AG886740 Oryza_sat
c 8	46.8	EST:*	8: gb_gbb1:*	2.6	CNS00LT2	CO886405	LM_SIS_00	CO886405 LM_SIS_00
c 9	46.8	EST:*	9: gb_gbb2:*	2.6	CNS00LT2	CO84976	LM_GRS_00	CO84976 LM_GRS_00
c 10	46.6	EST:*	10: gb_gbb3:*	2.6	CNS00LT2	CA741621	wif1c_Dko	CA741621 wif1c_Dko
c 11	46.6	EST:*	11: gb_gbb3:*	2.6	CNS00LT2	BP162319	BP162319	BP162319
c 12	46.6	EST:*	11: gb_gbb3:*	2.6	CNS00LT2	AL076720	Drosophil_bac.him.	AL076720 Drosophil_bac.him.
c 13	46.4	EST:*	11: gb_gbb3:*	2.6	CNS00LT2	CA222795	SCBZFL403	CA222795 SCBZFL403
c 14	46.4	EST:*	11: gb_gbb3:*	2.6	CNS00LT2	AW255255	ML252_pep	AW255255 ML252_pep
c 15	45.6	EST:*	12: gb_gbb3:*	2.6	CNS00LT2	CP953096	8886service	CP953096 8886service
c 16	45.6	EST:*	12: gb_gbb3:*	2.6	CNS00LT2	CP962795	7934service	CP962795 7934service
c 17	45.6	EST:*	12: gb_gbb3:*	2.6	CNS00LT2	CP962795	7773service	CP962795 7773service
c 18	45.6	EST:*	12: gb_gbb3:*	2.6	CNS00LT2	CP959714	7736service	CP959714 7736service
c 19	45.4	EST:*	12: gb_gbb3:*	2.6	CNS00LT2	DN145761	4836_G12	DN145761 4836_G12
c 20	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DR179060	RTWNT1_1	DR179060 RTWNT1_1
c 21	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DR012815	HRAT1_15	DR012815 HRAT1_15
c 22	45.2	EST:*	12: gb_gbb3:*	2.5	CNS00LT2	DN458173	EST933972	DN458173 EST933972

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 GenCore version 5.1.6
 I nucleic - nucleic search, using sw model
 on or: January 24, 2006, 01:18:23 ; Search time 1095 Seconds
 (without alignments)
 10/91-324 Million cell updates/sec
 title: US-10-808-964A-2
 perfect score: 1773
 sequence: 1 ggtacctcgatggattgttc.....caaatcgccctcggttacc 1773
 scoring table: IDENTITY NUC
 GapOp 10.0 , GapExt 1.0
 searched: 4996997 seqs, 3332346308 residues
 total number of hits satisfying chosen parameters: 9993994
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 post-processing: Minimum Match 0%
 Maximum Match 100%

```

database : N_Geneseq_21:*
 1: Genesegn1980s:*
 2: Genesegn1990s:*
 3: Genesegn2000s:*
 4: Genesegn2001as:*
 5: Genesegn2001bs:*
 6: Genesegn2002as:*
 7: Genesegn2002bs:*
 8: Genesegn2003as:*
 9: Genesegn2003bs:*
10: Genesegn2003cs:*
11: Genesegn2003ds:*
12: Genesegn2004as:*
13: Genesegn2004bs:*
14: Genesegn2005s:*

```

• 5

result	No.	Query	Score	Match	Length	DB	ID	Description	
								Ad57177	Porcine C
c	1	1773	100.0	1773	9	AAL57177		Ad57176	Pig_circus
c	2	1296.4	73.1	1767	13	ADN76756		Abx08205	PMWS_Porc
c	3	1285.2	72.5	1768	6	ABX0205		Abx08203	PMWS_Porc
c	4	1278.8	72.1	1768	6	ABX0203		Abx08207	CT_Porcin
c	5	1277.2	72.0	1768	6	ABX0207		Abx08206	CT_Porcin
c	6	1274	71.9	1768	6	ABX0206		Abx08204	PMWS_Porc
c	7	1274	71.9	1768	6	ABX0204		Abx08219	PMWS_Porc
c	8	1270.8	71.7	1774	6	ABX0219		Abx08202	PMWS_Porc
c	9	1252	70.6	1762	6	ABX0202		Abx08208	CT_Porcin
c	10	1218.2	68.7	1759	6	ABX0308		Abx08220	PK-15_Por
c	11	1210.4	68.3	1759	6	ABX0320		Aah74867	Nucleotid
c	12	1196.8	67.5	7460	4	AAH74867		Abx94361	Rolling_C
c	13	1196.8	67.5	7460	8	ABX9461		Aah74865	Nucleotid
c	14	1195.8	67.4	5285	4	AAH74855		Abx94355	Rolling_C
c	15	1195.8	67.4	5285	8	ABX94355		Aah74866	Nucleotid
c	16	1195.8	67.4	5650	4	AAH74866		Abx94356	Rolling_C
c	17	1195.8	67.4	5650	8	ABX94356		Aaf75839	DNA_fragm
c	18	1059.4	59.7	1759	4	AAF75839		Aal57176	Porcine C
c	19	1058.4	59.7	1768	9	AAL57176			

RESULT 1	
AAL57177	AAL57177 standard; DNA; 1773 BP.
ID	
XX	
AC	AAL57177;
XX	
DT	27-OCT-2003 (revised)
DT	09-OCT-2003 (first entry)
XX	
DE	Porcine circovirus type 1-2 chimeric DNA.
XX	Porcine circovirus type 2; PCV1-2; PCV2; PMWS; weaning piglet; dyspnoea; progressive weight loss; postweaning multisystemic wasting syndrome; ds; tachypnoea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene; viral infection; chimeric.
KW	
XX	
OS	Porcine circovirus type 1.
OS	Porcine circovirus type 2.
OS	Chimeric.

ALIGNMENTS

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OM nucleic - nucleic search, using sw model 1

Run on: January 24, 2006, 04:27:51 ; Search time 9027 seconds

(without alignments)

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtacccctccggatgttc.....caaatacgcccttcgggtacc 1773

Scoring table: IDENTITY_NUC GAP0 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
 1: gb:ba:
 2: gb:in:
 3: gb:env:
 4: gb:om:
 5: gb:ov:
 6: gb:bat:
 7: gb:ph:
 8: gb:pr:
 9: gb:ro:
 10: gb:sts:
 11: gb:sv:
 12: gb:un:
 13: gb:vi:
 14: gb:htg:
 15: gb:pl:
 16: gb:nc:
 17: gb:ncip:
 18: gb:ncip:
 19: gb:ncip:
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 42: gb:ncip:
 43: gb:ncip:
 44: gb:ncip:
 45: gb:ncip:

AY288134 Porcine c
 AY294310 Porcine c
 AY288133 Porcine c
 AX379562 Sequence
 AY099498 Porcine c
 AX379560 Sequence
 AY099496 Porcine c
 AX379564 Sequence
 AY09500 Porcine c
 AX379561 Sequence
 AX379563 Sequence
 AY09495 Porcine c
 AY09499 Porcine c
 Y0921 Porcine cir
 AP05532 Porcine c
 AX379559 Sequence
 AY09497 Porcine c
 AX379565 Sequence
 AY099501 Porcine c
 AX226286 Sequence
 AX226281 Sequence
 A97282 Sequence 5
 AR145612 Sequence
 BD081867 Porcine c
 CQ768117 Sequence

ALIGNMENTS

RESULT 1
 LOCUS AF264042_c
 DEFINITION Porcine circovirus type 2 isolate 40895 complete genome.
 ACCESSION AF264042
 VERSION AF264042.1 GI:9392644
 KEYWORDS
 SOURCE Porcine circovirus 2
 ORGANISM Porcine circovirus 2
 VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
 REFERENCE 1 (bases 1 to 1768)
 AUTHORS Penaux, M., Halbur, P.G., Gill, M., Toth, T.B. and Meng, X.J.
 TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
 J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
 JOURNAL
 PUBLISHED 10878032
 REFERENCES Penaux, M., Halbur, P.G., Gill, M., Toth, T.B. and Meng, X.J.
 AUTHORS
 TITLE Direct Submission
 JOURNAL Submitted (08-MAY-2000) VNRCCM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
 FEATURES
 Source
 Location/Qualifiers
 1. 1768
 /organism="Porcine circovirus 2"
 /mol_type="genomic DNA"
 /isolate="40895"
 /db_xref="taxon:85708"
 /complement(37..738)
 /gene="cap"
 /complement(1 to 1768)
 /gene="cap"
 /note="Cap"
 /codon_start=1
 /product="putative capsid protein"
 /protein_id="AAPB72351"
 /db_xref="GI:9392645"
 /translation="MTIPRRYRRRRHPRSHLQILARRPMLVPHRYMRKQGJ
 FNTRLSSRFGTIVKATTVRTPSWAVDMRMRNFTDDFVPGGTNKNISIPEFYTRKVK"

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
C 1	1386.4	78.2	1768	13	AF264042	Porcine c	AF264042 Porcine c
C 2	1378.4	77.7	1768	13	AP264040	Porcine c	AP264040 Porcine c
C 3	1370.4	77.3	1768	13	AP264039	Porcine c	AP264039 Porcine c
C 4	1370.4	77.3	1768	13	AF520783	Porcine c	AF520783 Porcine c
C 5	1370.4	77.3	1768	13	AP544024	Porcine c	AP544024 Porcine c
C 6	1368.8	77.2	1768	13	AP264041	Porcine c	AP264041 Porcine c
C 7	1367.2	77.1	1768	13	AF264038	Porcine c	AF264038 Porcine c
C 8	1354.2	76.9	1768	13	AP264043	Porcine c	AP264043 Porcine c
C 9	1354.2	76.9	1768	13	AP54546	Porcine c	AP54546 Porcine c
C 10	1357.6	76.6	1768	13	AF201309	Porcine c	AF201309 Porcine c
C 11	1346.4	75.9	1768	13	AP201305	Porcine c	AP201305 Porcine c
C 12	1346.4	75.9	1768	13	AP201308	Porcine c	AP201308 Porcine c
C 13	1343.2	75.8	1768	13	AF201306	Porcine c	AF201306 Porcine c
C 14	1341.6	75.7	1768	13	AP201310	Porcine c	AP201310 Porcine c
C 15	1340.6	75.6	1768	13	AF201307	Porcine c	AF201307 Porcine c
C 16	1306.7	73.7	1767	11	AJ623306	Synthetic	AJ623306 Synthetic
C 17	1304.4	73.6	1767	13	AF201311	Porcine c	AF201311 Porcine c
C 18	1303.4	73.5	1767	13	AY122275	Porcine c	AY122275 Porcine c